1154	c1153	1152	1151	1150	C1149	C1148	C1147	c1146	c1145	C1144	1143	1142	C1141	C1140	1139	c1138	1137	c1136	c1135	1134	c1133	c1132	C1131	1130	c1129
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ABI99093	AAD26058	AAD26043	AAD26754	ABK54455 :	ABK72343	ABS64182	AAF53602	AAF53601	AAF53600	AAF53599	AAF48796	AAF48795	AAF81549	AAH23587	AAH55212	AAH55211	AAH55208	AAH55207	AAI71747	AA167276	AAZ90118	AAX28221	AAV57003	AAT46990	AAT52130
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Human PCDH2 ASO PC	Human apolipoprote	Human apolipoprote	Human SNAP29 gene	ASO primer #5 to d	Human HTR5A gene a	Tachykinin recepto	IGF-I oligonucleot	<pre>IGF-I oligonucleot</pre>	н	IGF-I oligonucleot	IGFBP3 oligonucleo	IGFBP3 oligonucleo	Dye-labeled molecu			DNA	Genomic DNA methyl	DNA	PCR primer #2. Sy	Human FKBP8 allele	PCR primer H-T11A	Tumour antigen ant	Human Notch3 gene	HLA sequence 29.	Human ICAM hammerh

ALIGNMENTS

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RESULT 1
ABZ0175
ID ABZ0
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XX ABZ0
XX ABZ0
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XX PHuma
XX T7;
XW athe
XX PPT WOA!
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08-JUN-2001; 2001US-296764P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  rheumatoid arthritis, osteoarthritis or cytomegalovirus infection.
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                                               1385 GCCTTCATGCACCTGTCCTTTCTAACACGTCGCCTTCAACTGTAATCACA
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GCCTTCATGCACCTGTCCTTTCTAACACGTCGCCTTCAACTGTAATCACA
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llarity 100.0%;
Conservative
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ABZ04679
ID ABZC 09-JAN-2003 ABZ04679 standard; DNA; 50 BP

Human leukocyte gene expression profiling probe SEQ ID NO

(first entry)

T7; leukocyte; gene expression profiling; allograft rejection; atherosclerosis; congestive heart failure; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe; . 89

Homo sapiens.

WO200257414-A2

25-JUL-2002

22-OCT-2001; 2001WO-US47856

20-OCT-2000; 2000US-241994P. 08-JUN-2001; 2001US-296764P.

(BIOC-) BIOCARDIA INC

Wohlgemuth J, Woodward Fry K, Matcuk G, ...
d R, Quertermous T, Altman P, Iohnson ۲ij ۲۰ Prentice Phillips

J,

New system for leukocyte expression profiling, diagnosing a disease, or monitoring (the rate of) progression of a disease, e.g. atherosclerosis or congestive heart failure, comprises diagnostic oligonucleotides

Claim 1; Page 477; 2038pp; English.

The invention relates to a system for detecting gene expression, which comprises one or two isolated DNA molecules that detect expression of a gene, where the gene corresponds to any of 8143 oligonucleotides (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful for leukocyte expression profiling. It is particularly useful for diagnosing a disease, monitoring (rate of) progression of a disease, predicting therapeutic outcome, determining prognosis for a patient, predicting disease complications in an individual or monitoring response to treatment in an individual or monitoring response to treatment in an individual or monitoring response to treatment in an individual or the disease include cardiac allograft rejection, kidney allograft rejection, liver allograft rejection, the cardiac allograft rejection, some some particular or the property of the systemic lupus erythematosus, the property of the systemic lupus erythematosus, the property of the systemic lupus erythematosus. rheumatoid arthritis, osteoarthritis or cytomegalovirus infection.

New system for leukocyte expression profiling, diagnosing a disease, or monitoring (the rate of) progression of a disease, e.g. atherosclerosis or congestive heart failure, comprises diagnostic oligonucleotides

WPI; 2002-636525/68.

Ly N, Wohlgemuth J,

muth J, Fry Woodward R,

K, Matcuk G, Quertermous

'n,

Altman P, Johnson

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Phillips

(BIOC-) BIOCARDIA INC

The invention relates to a system for detecting gene expression, comprises one or two isolated DNA molecules that detect expressi gene, where the gene corresponds to any of 8143 oligonucleotides

expression

1; Page 332; 2038pp; English

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RESULT 3
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                                                                                          The present invention relates to human oligonucleotides comprising single nucleotide polymorphic site (SNP: AAH89797-AAH89219). The presequence is one such oligonucleotide. The oligonucleotides can be uforensics, paternity testing, correlation of polymorphisms with phenotypic traits, genetic mapping of phenotypic traits and marker assisted breeding of animals and crop plants.
                                                                                                                                                                                  New polymorphic sites derived from the human genome are useful to determine sites correlating with phenotypic traits, particularly disease, and also in forensics and paternity testing
                                                                           Sequence
                                                                                                                                                                 Claim 37;
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                                                                                                                                                                                                                           WPI; 2001-335945/35
                                                                                                                                                                                                                                                                                              10-NOV-1999;
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plant breeding;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                        WO200134840-A2
                                                                                                                                                                                                                                                                                                                                                                                                Variation
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                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; single nucleotide polymorphic; SNP; forensic science;
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                  979
                                     21;
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AFFYMETRIX INC.
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             TGCAGTGCCCCCTAAGTGACC
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eding; ds.
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                                   3.9%; Sullarity 100.0%; I Conservative 0;
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larity 100.0%;
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0.00018;
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28;
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RESULT 4

Homo sapiens

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ARESULT 5
AAC96345/c
ID AAC963
XX AAC963
XX AAC963
XX DT 26-FEB
XX HLA DP
DE HLA DP
DE HLA DP
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                    DNA sequence analysis; sequencing; protein sequence; protein structure; gene typing; organ donation; bacteria identification; 16s rRNA; HLA; human leukocyte antigen; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                New polymorphic sites derived from the human genome are useful to determine sites correlating with phenotypic traits, particularly disease, and also in forensics and paternity testing
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Variation
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                                                                    HLA DPB1 gene
                                                                                            26-FEB-2001
                                                                                                                    AAC96345;
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(AFFY-)
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AFFYMETRIX INC.
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                                                                                                                                                                                                     ATAACGTTTCCGGTATTACTC
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                                                                     PCR primer #77.
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replace(11,t)
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                                                                                                                                           DNA;
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RESULT 6
AAQ75716/c
ID AAQ75716;
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AC AAQ75716;
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DE Reverse tr
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DE Reverse tr
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Analysis;
KW Analysis;
KW aggregate;
XX
Synthetic.
XX
Synthetic.
XX
PF 16-APR-19;
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PF 16-APR-19;
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PR 16-APR-19;
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PR (NITE) N:
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PR WPI; 1995.
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PR Analysis;
PT Analysis;
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                                                                                                                                                                                                                                                                                                                                        01-NOV-1994
                            Disclosure;
                                                                                                                                              WPI; 1995-018287/03.
                                                                                                                                                                                                                                             16-APR-1993;
                                                                                                                                                                                                                                                                                          16-APR-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aggregate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reverse transcription primer used in cDNA analysis technique
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides a method for identifying a set of extendible primers which can be used in the identification, typing and classification of genes. This can then be used to predict protein sequence and structure, in organ donation to match the organ with the receiver, and to identify bacteria in a sample. The method can be used type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ulfendahl P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Analysis;
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                                                                                                                                                                                          (NITE ) NIPPON TELEGRAPH & TELEPHONE
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les 21; Conserv
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by
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                      Page
                                                                    cDNA and gene expression - digestion with restriction
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                 8; 11pp; Japanese
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enzyme; ss.
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Pred. No. 6
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ATGCTAAAAAAAAAAAAA 1496 |||| |||||||||||||| ATGCAAAAAAAAAAAAAAA 1 Query Match Best Local Matches 2

Similarity

95.2%;

Score 19.4; Pred. No. 63;

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                                                                     A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression residuals.
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     Sequence
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                                                                                                                                                                                                                                                                                                                      Disclosure; Page 6; llpp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-APR-1993;
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  1 A;
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n with restriction
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  C; 1 G; 18
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Pred. No.
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  other;
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47;
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RESULT 9
AAQ75578/c
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XX AAQ755
XX O4-AUG
DT O4-AUG
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid isolate encoding flavonoid-3'-hydroxylase create transgenic plants with altered petal colour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-MAR-1992;
07-JAN-1993;
                                                                                                                                                                                                                                                                  04-AUG-1995
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27-APR-1994
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16-APR-1993;
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                                      01-NOV-1994.
                                                                                                                                                              aggregate;
                                                                                                                                                                               Analysis; gene expression; reverse transcription; primer; cDNA;
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                                                                                                                                                              restriction
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP; 1 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Holton
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93AU-0006698.
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100.0%; Er
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of a PCR primer which was used in polymerase the amplification of cloned cytochrome P450
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                                                                                                                                                            enzyme;
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in separate lanes. The method can be used to analyse gene expression
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                                                                                                                                                                                                         Analysis of cDNA and gene expression - followed by digestion with restriction
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